

4-31452A.ST25.txt  
SEQUENCE LISTING

<110> Novartis AG

<120> Adenovirus particles with mutagenized fiber proteins

<130> 4-31452A

<160> 43

<170> PatentIn version 3.0

<210> 1

<211> 1746

<212> DNA

<213> Human adenovirus type 5

<220>

<221> CDS

<222> (1)..(1746)

<400> 1

atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96  
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20

25

30

44

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  
1  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35

40

45

92

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  
1  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50

55

60

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

## 4-31452A.ST25.txt

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu

180

185

190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr

210

215

220

ggc cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr

225

230

235

240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala

245

250

255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val

260

265

270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

## 4-31452A.ST25.txt

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
 12  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
 60  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
 08  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
 56  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
 04  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
 52  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
 00

## 4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

ttg tgg acc aca cca gct cca tct oct aac tgt aga cta aat gca gag 12

48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12

96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420 425 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13

44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13

92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14

40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14

88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15

## 4-31452A.ST25.txt

36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15  
 84  
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16  
 32  
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16  
 80  
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
 545 550 555 560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17  
 28  
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
 565 570 575

tac att gcc caa gaa taa 17  
 46  
 Tyr Ile Ala Gln Glu

580

<210> 2  
 <211> 581  
 <212> PRT  
 <213> Human adenovirus type 5  
 <400> 2

4-31452A.ST25.txt

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

4-31452A.ST25.txt

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
565 570 575

4-31452A.ST25.txt

Tyr Ile Ala Gln Glu  
580

<210> 3  
<211> 1746  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>  
<221> CDS  
<222> (1)..(1746)

<220>  
<221> mutation  
<222> (1222)..(1227)

<400> 3  
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15

56  
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96  
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

70  
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1  
44  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

80  
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1  
92  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80  
  
 caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95  
  
 ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110  
  
 act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125  
  
 atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140  
  
 gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160  
  
 aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

## 4-31452A.ST25.txt

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

## 4-31452A.ST25.txt

275

280

285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
 12  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

290

295

300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
 60  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu

305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
 08  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile

325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
 56  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro

340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
 04  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp

355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
 52  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp

370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
 00

## 4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag 12  
48

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu

405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12  
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420 425 430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13  
44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435 440 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13  
92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450 455 460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14  
40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465 470 475 480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14  
88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485 490 495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15

## 4-31452A.ST25.txt

36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15  
84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16  
32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16  
80

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17  
28

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa

46

Tyr Ile Ala Gln Glu

580

&lt;210&gt; 4

&lt;211&gt; 581

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;400&gt; 4

4-31452A.ST25.txt

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

4-31452A.ST25.txt

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
565 570 575

4-31452A.ST25.txt

Tyr Ile Ala Gln Glu  
580

<210> 5  
<211> 1740  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 441(V) & 442(K) of wild-type fiber were deleted

<220>  
<221> CDS  
<222> (1)..(1740)

<400> 5  
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96  
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct 1  
44  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc 1  
92  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr

## 4-31452A.ST25.txt

165

170

175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln

## 4-31452A.ST25.txt

275	280	285	
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn			9
290	295	300	
aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu			9
305	310	315	320
gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile			10
325	330	335	
gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro			10
340	345	350	
aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 04 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp			11
355	360	365	
tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 52 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp			11
370	375	380	
agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 00			12

## 4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12  
48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405 410 415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12  
96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420 425 430

ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga 13  
44

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly

435 440 445

aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg 13  
92

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val

450 455 460

cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat 14  
40

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

465 470 475 480

gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg 14  
88

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met

485 490 495

cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt

## 4-31452A.ST25.txt

36

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser  
 500 505 510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 15  
 84

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val  
 515 520 525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 16  
 32

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr  
 530 535 540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16  
 80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn  
 545 550 555 560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17  
 28

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile  
 565 570 575

gcc caa gaa taa 17

40

Ala Gln Glu

<210> 6  
 <211> 579  
 <212> PRT  
 <213> Artificial

<400> 6

4-31452A.ST25.txt

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

4-31452A.ST25.txt

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
195 200 205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

4-31452A.ST25.txt

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr  
385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly  
435 440 445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val  
450 455 460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn  
465 470 475 480

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met  
485 490 495

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser  
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val  
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr  
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn  
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile  
565 570 575

Ala Gln Glu

<210> 7  
 <211> 1740  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Codes for a mutated Human Adenovirus type 5 fiber protein. Comb  
 in  
 ation of the mutant fiber encoded in Seq ID: #3 & 5

<220>  
 <221> CDS  
 <222> (1)..(1740)

<400> 7			
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca			
48			
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro			
1	5	10	15
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc			
96			
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro			
20	25	30	
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct			1
44			
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser			
35	40	45	
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc			1
92			
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu			
50	55	60	

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc	2		
40			
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser			
65	70	75	80
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac	2		
88			
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn			
85	90	95	
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta	3		
36			
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu			
100	105	110	
act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc	3		
84			
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr			
115	120	125	
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att	4		
32			
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile			
130	135	140	
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa	4		
80			
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln			
145	150	155	160
aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act	5		
28			
Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr			
165	170	175	

## 4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

## 4-31452A.ST25.txt

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
 12  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
 60  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
 08  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
 56  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
 04  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
 52  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
 00  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

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## 4-31452A.ST25.txt

385

390

395

400

ttg tgg acc aca cca gct cca gag gct aac tgt aga cta aat gca gag 12  
 48

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12  
 96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gcc ggc agt ttg gct cca ata tct gga 13  
 44

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly

435

440

445

aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg 13  
 92

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val

450

455

460

cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga aat 14  
 40

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn

465

470

475

480

gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg 14  
 88

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met

485

490

495

cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt 15  
 36

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser

4-31452A.ST25.txt

500

505

510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 15  
84

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

515

520

525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 16  
32

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16  
80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17  
28

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa

40

Ala Gln Glu

17

<210> 8

<211> 579

<212> PRT

<213> Artificial

<400> 8

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

## 4-31452A.ST25.txt

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

## 4-31452A.ST25.txt

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

## 4-31452A.ST25.txt

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Glu Ala Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Gly Ser Leu Ala Pro Ile Ser Gly  
435 440 445

Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val  
450 455 460

Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn  
465 470 475 480

Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met  
485 490 495

Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser  
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val  
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr  
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn  
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile  
565 570 575

Ala Gln Glu

<210> 9  
<211> 1743  
<212> DNA  
<213> Artificial  
  
<220>  
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acid 441(V) of wild-type fiber was deleted  
  
<220>  
<221> CDS  
<222> (1)..(1743)  
  
<400> 9  
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15  
  
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30  
  
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  
44 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
1 35 40 45  
  
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  
92 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

## 4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

## 4-31452A.ST25.txt

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
 12  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
 60  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
 08  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
 56  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
 04  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
 52  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
 00  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

## 4-31452A.ST25.txt

385	390	395	400
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12			
48			
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
405 410 415			
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12			
96			
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
420 425 430			
ctt gct aca gtt tca gtt ttg gct aaa ggc agt ttg gct cca ata tct 13			
44			
Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser			
435 440 445			
gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga 13			
92			
Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly			
450 455 460			
gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga 14			
40			
Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg			
465 470 475 480			
aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt 14			
88			
Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe			
485 490 495			
atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa 15			
36			
Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys			

## 4-31452A.ST25.txt

500

505

510

agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct 15  
84

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro

515

520

525

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca 16  
32

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

530

535

540

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac 16  
80

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545

550

555

560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac 17  
28

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

565

570

575

att gcc caa gaa taa

43

Ile Ala Gln Glu

580

&lt;210&gt; 10

&lt;211&gt; 580

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;400&gt; 10

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
 20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
 50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

4-31452A.ST25.txt

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
 405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
 420 425 430

Leu Ala Thr Val Ser Val Leu Ala Lys Gly Ser Leu Ala Pro Ile Ser  
 435 440 445

Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly  
 450 455 460

Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg  
 465 470 475 480

Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe  
 485 490 495

Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys  
 500 505 510

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro  
 515 520 525

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr  
 530 535 540

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His  
 545 550 555 560

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr  
 565 570 575

Ile Ala Gln Glu

<210> 11  
<211> 1743  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc  
le  
otides corresponding to amino acid 442(K) of wild-type fiber wa  
s  
deleted

<220>  
<221> CDS  
<222> (1)..(1743)

<400> 11  
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15  
  
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96  
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30  
  
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  
44 1  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45  
  
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  
92 1  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

## 4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

## 4-31452A.ST25.txt

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
 12  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
 60  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
 08  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
 56  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
 04  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
 52  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
 00  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

## 4-31452A.ST25.txt

385	390	395	400	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12				
48				
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu				
405 410 415				
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12				
96				
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile				
420 425 430				
ctt gct aca gtt tca gtt ttg gct gtt ggc agt ttg gct cca ata tct 13				
44				
Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser				
435 440 445				
gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga 13				
92				
Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly				
450 455 460				
gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt aga 14				
40				
Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg				
465 470 475 480				
aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt 14				
88				
Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe				
485 490 495				
atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa 15				
36				
Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys				

## 4-31452A.ST25.txt

500

505

510

agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct 15  
 84

Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro

515

520

525

gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca 16  
 32

Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr

530

535

540

act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac 16  
 80

Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His

545

550

555

560

aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac 17  
 28

Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr

565

570

575

att gcc caa gaa taa 17

43

Ile Ala Gln Glu

580

&lt;210&gt; 12

&lt;211&gt; 580

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;400&gt; 12

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

## 4-31452A.ST25.txt

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

biochem 30207360

4-31452A.ST25.txt

385	390	395	400
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu			
405	410	415	
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile			
420	425	430	
Leu Ala Thr Val Ser Val Leu Ala Val Gly Ser Leu Ala Pro Ile Ser			
435	440	445	
Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly			
450	455	460	
Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg			
465	470	475	480
Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe			
485	490	495	
Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys			
500	505	510	
Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro			
515	520	525	
Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr			
530	535	540	
Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His			
545	550	555	560
Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr			
565	570	575	
Ile Ala Gln Glu			

<210> 13  
<211> 1746  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>  
<221> CDS  
<222> (1)..(1746)

<220>  
<221> mutation  
<222> (1321)..(1326)

<400> 13  
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1 5 10 15

5 96  
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96  
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  
44 1  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  
92 1  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

## 4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

## 4-31452A.ST25.txt

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
 12  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
 60  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
 08  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
 56  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
 04  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
 52  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
 00  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

## 4-31452A.ST25.txt

385	390	395	400	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12				
48				
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu				
405 410 415				
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12				
96				
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile				
420 425 430				
ctt gct aca gtt tca gtt ttg gct gct gca ggc agt ttg gct cca ata 13				
44				
Leu Ala Thr Val Ser Val Leu Ala Ala Gly Ser Leu Ala Pro Ile				
435 440 445				
tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13				
92				
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn				
450 455 460				
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14				
40				
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe				
465 470 475 480				
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14				
88				
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly				
485 490 495				
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15				
36				
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala				

## 4-31452A.ST25.txt

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15  
 84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16  
 32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16  
 80

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17  
 28

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa

46

Tyr Ile Ala Gln Glu

580

&lt;210&gt; 14

&lt;211&gt; 581

&lt;212&gt; PRT

&lt;213&gt; Artificial

&lt;400&gt; 14

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

## 4-31452A.ST25.txt

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

09320202-052001

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
 405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
 420 425 430

Leu Ala Thr Val Ser Val Leu Ala Ala Ala Gly Ser Leu Ala Pro Ile  
 435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
 450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
 545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
 565 570 575

Tyr Ile Ala Gln Glu

<210> 15  
<211> 1746  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a mutated Human Adenovirus type 5 fiber protein.

<220>  
<221> CDS  
<222> (1)..(1746)

<220>  
<221> mutation  
<222> (1378)..(1380)

<400> 15  
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15

5 10 15  
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96  
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro

20 25 30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  
44 1  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser

35 40 45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  
92 1  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu

50 55 60

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

## 4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg	5		
76			
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu			
180	185	190	
aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg	6		
24			
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly			
195	200	205	
gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act	6		
72			
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr			
210	215	220	
ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act	7		
20			
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr			
225	230	235	240
gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca	7		
68			
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala			
245	250	255	
gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt	8		
16			
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val			
260	265	270	
agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag	8		
64			
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln			
275	280	285	

## 4-31452A.ST25.txt

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
 12  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
 60  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
 08  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
 56  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
 04  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
 52  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
 00  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

## 4-31452A.ST25.txt

385	390	395	400	
ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12				
48				
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu				
405 410 415				
aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12				
96				
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile				
420 425 430				
ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13				
44				
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile				
435 440 445				
tct gga aca gtt caa agt gct cat ctt att ata gaa ttc gac gaa aat 13				
92				
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn				
450 455 460				
gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14				
40				
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe				
465 470 475 480				
aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14				
88				
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly				
485 490 495				
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15				
36				
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala				

4-31452A.ST25.txt

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15  
84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac 16  
32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp

530

535

540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc 16  
80

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly

545

550

555

560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca 17  
28

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser

565

570

575

tac att gcc caa gaa taa

46

Tyr Ile Ala Gln Glu

580

<210> 16

<211> 581

<212> PRT

<213> Artificial

<400> 16

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

## 4-31452A.ST25.txt

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
 405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
 420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
 435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Glu Phe Asp Glu Asn  
 450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp  
 530 535 540

Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly  
 545 550 555 560

His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser  
 565 570 575

Tyr Ile Ala Gln Glu

<210> 17  
<211> 1740  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nucleotides corresponding to amino acids 509(G) & 510(K) of wild-type fiber were deleted

<220>  
<221> CDS  
<222> (1)..(1740)

<400> 17  
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15

1  
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96  
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

1  
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  
44  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

1  
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  
92  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

## 4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

## 4-31452A.ST25.txt

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
 12  
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
 290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
 60  
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
 305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
 08  
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
 325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
 56  
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
 340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
 04  
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
 355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
 52  
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
 370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
 00  
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

## 4-31452A.ST25.txt

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12  
 48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12  
 96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13  
 44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13  
 92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14  
 40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14  
 88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac act gcc aaa agt 15  
 36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser

4-31452A.ST25.txt

500

505

510

aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta 15  
84

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val

515

520

525

aca cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act 16  
32

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16  
80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17  
28

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa

40

Ala Gln Glu

17

<210> 18

<211> 579

<212> PRT

<213> Artificial

<400> 18

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

09870203-053001

## 4-31452A.ST25.txt

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

## 4-31452A.ST25.txt

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

## 4-31452A.ST25.txt

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Thr Ala Lys Ser  
500 505 510

Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val  
515 520 525

Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr  
530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn  
545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile  
565 570 575

Ala Gln Glu

<210> 19  
<211> 1740  
<212> DNA  
<213> Artificial

<220>  
<223> Codes for a mutated Human Adenovirus type 5 fiber protein. Nuc  
le  
otides corresponding to amino acids 538(G) & 539(T) of wild-typ  
e  
fiber were deleted

<220>  
<221> CDS  
<222> (1)..(1740)

<400> 19  
atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca  
48  
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro  
1 5 10 15  
  
tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc  
96  
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30  
  
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct  
44  
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45  
  
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc  
92  
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

## 4-31452A.ST25.txt

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc 2  
 40  
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
 65 70 75 80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac 2  
 88  
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
 85 90 95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta 3  
 36  
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
 100 105 110

act gtg gct gcc gca cct cta atg gtc gcg ggc aac aca ctc acc 3  
 84  
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
 115 120 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att 4  
 32  
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
 130 135 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa 4  
 80  
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
 145 150 155 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 5  
 28  
 Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
 165 170 175

## 4-31452A.ST25.txt

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 5  
 76  
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
 180 185 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 6  
 24  
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly  
 195 200 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 6  
 72  
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
 210 215 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 7  
 20  
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
 225 230 235 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 7  
 68  
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
 245 250 255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 8  
 16  
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
 260 265 270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 8  
 64  
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
 275 280 285

4-31452A.ST25.txt

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 9  
12 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 9  
60 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata 10  
08 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 10  
56 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat 11  
04 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac 11  
52 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 12  
00 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

## 4-31452A.ST25.txt

385

390

395

400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag 12  
 48

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu

405

410

415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata 12  
 96

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile

420

425

430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata 13  
 44

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile

435

440

445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat 13  
 92

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn

450

455

460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt 14  
 40

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe

465

470

475

480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga 14  
 88

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly

485

490

495

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc 15  
 36

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala

## 4-31452A.ST25.txt

500

505

510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa 15  
 84

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys

515

520

525

cct gta aca cta acc att aca cta aac cag gaa aca gga gac aca act 16  
 32

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr

530

535

540

cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac 16  
 80

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn

545

550

555

560

tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att 17  
 28

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile

565

570

575

gcc caa gaa taa  
 40

Ala Gln Glu

17

<210> 20  
 <211> 579  
 <212> PRT  
 <213> Artificial  
 <400> 20

Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro

1

5

10

15

Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro  
20 25 30

Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
35 40 45

Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu  
50 55 60

Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser  
65 70 75 80

Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn  
85 90 95

Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu  
100 105 110

Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr  
115 120 125

Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile  
130 135 140

Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln  
145 150 155 160

Thr Ser Gly Pro Leu Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr  
165 170 175

Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu  
180 185 190

Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly

## 4-31452A.ST25.txt

195

200

205

Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr  
210 215 220

Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr  
225 230 235 240

Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala  
245 250 255

Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val  
260 265 270

Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln  
275 280 285

Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn  
290 295 300

Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu  
305 310 315 320

Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile  
325 330 335

Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro  
340 345 350

Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp  
355 360 365

Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp  
370 375 380

Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr

385 390 395 400

Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu  
 405 410 415

Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile  
 420 425 430

Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile  
 435 440 445

Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn  
 450 455 460

Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe  
 465 470 475 480

Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly  
 485 490 495

Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala  
 500 505 510

Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys  
 515 520 525

Pro Val Thr Leu Thr Ile Thr Leu Asn Gln Glu Thr Gly Asp Thr Thr  
 530 535 540

Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn  
 545 550 555 560

Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile  
 565 570 575

Ala Gln Glu

<210> 21  
<211> 38  
<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(38)  
  
<400> 21  
accacaccag ctccagaggc taactgtaga ctaaatgc  
38  
  
<210> 22  
<211> 38  
<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(38)  
  
<400> 22  
gcatttagtc tacagttagc ctctggagct ggtgtgtt  
38  
  
<210> 23  
<211> 38  
<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(38)

## 4-31452A.ST25.txt

<400> 23  
acagtttcag ttttggccgg cagtttgct ccaatatc  
38

<210> 24  
<211> 38  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(38)

<400> 24  
gatattggag ccaaactgcc ggccaaaact gaaactgt  
38

<210> 25  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(36)

<400> 25  
acagtttcag ttttggctaa aggcagttg gctcca  
36

<210> 26  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

## 4-31452A.ST25.txt

<220>  
<221> primer\_bind  
<222> (1)..(36)

<400> 26  
tggagccaaa ctgccttag ccaaaaactga aactgt  
36

<210> 27  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(36)

<400> 27  
gtttagttt tggctgttgg cagtttgct ccaata  
36

<210> 28  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(36)

<400> 28  
tattggagcc aaactgccaa cagccaaaac tgaaac  
36

<210> 29  
<211> 36  
<212> DNA  
<213> Artificial

4-31452A.ST25.txt

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(36)

<400> 29  
gttgcagttt tggctgctgc aggcaagttt gctcca  
36

<210> 30  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(36)

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36

<210> 31  
<211> 36  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(36)

<400> 31  
gctcatctta ttatagaatt cgacgaaaat ggagtg  
36

<210> 32  
<211> 36

4-31452A.ST25.txt

<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(36)  
  
<400> 32  
cactccattt tcgtcgaatt ctataataag atgagc  
36  
  
<210> 33  
<211> 39  
<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(39)  
  
<400> 33  
gcttatccaa aatctcacac tgccaaaagt aacattgtc  
39  
  
<210> 34  
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<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(39)  
  
<400> 34  
gacaatgtta cttttggcag tgtgagattt tggataagc  
39

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<210> 35  
<211> 35  
<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(35)  
  
<400> 35  
ctaaccatta cactaaacca ggaaacagga gacac  
35  
  
<210> 36  
<211> 35  
<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(35)  
  
<400> 36  
gtgtctcctg tttcctggtt tagtgtaatg gttag  
35  
  
<210> 37  
<211> 33  
<212> DNA  
<213> Artificial  
  
<220>  
<223> PCR primer  
  
<220>  
<221> primer\_bind  
<222> (1)..(33)  
  
<400> 37

4-31452A.ST25.txt

ataagatttg acgaaactgg agtgctacta aac  
33

<210> 38  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(33)

<400> 38  
gttagtagc actccagttt cgtcaaatct tat  
33

<210> 39  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(33)

<400> 39  
tttacgaaa atggacacct actaaacaat tcc  
33

<210> 40  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind

4-31452A.ST25.txt

<222> (1)..(33)

<400> 40  
ggaattgttt agtaggtgtc cagtttcgtc aaa  
33

<210> 41  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(33)

<400> 41  
aacctatcag cttatgcaaa atctcacggt aaa  
33

<210> 42  
<211> 32  
<212> DNA  
<213> Artificial

<220>  
<223> PCR primer

<220>  
<221> primer\_bind  
<222> (1)..(32)

<400> 42  
tttaccgtga gattttgcat aagctgatag gt  
32

<210> 43  
<211> 10  
<212> PRT  
<213> Artificial

<220>  
<223> cRGD consensus sequence

4-31452A.ST25.txt

<400> 43

His Cys Asp Cys Arg Gly Asp Cys Phe Cys  
1 5 10

00000000000000000000000000000000